

Oy	121	RFRFRFRGKHHSHFHDVLFVLEKKNYTPADADNDENPASHRYLYMAYTKYKTYTANDEF	180
Dp	121	RFRMRFRGKHHSHFHDVLFVLEKKNYTPADADNDENPASHRYLYMAYTKYKTYTANDEF	180
Oy	181	GASFPNKLSFTTGLFGWGIKRALKOIIRSNLPDIDGTEHSHVSRLOHTSSYKDYMDTOIP	240
Dp	181	GASFPNKLSFTTGLFGWGIKRALKOIIRSNLPDIDGTEHSHVSRLOHTSSYKDYMDTOIP	240
Oy	241	ALPKRKRFRSLMVVORCLLATYAGVYDPIPMWKKYMKLKNFVNVNVEFPTPKKFFKEIREP	300
Dp	241	ALPKRKRFRSLMVVORCLLATYAGVYDPIPMWKKYMKLKNFVNVNVEFPTPKKFFKEIREP	300
Oy	301	SKALKEKYSTDTKOLFENKIGQVDFEFNKETIRDPSSALKEKYSNDKKDLFENKIGQTV	360
Dp	301	SKALKEKYSTDTKOLFENKIGQVDFEFNKETIRDPSSALKEKYSNDKKDLFENKIGQTV	360
Oy	361	DFINNEIRDPSSKALIRKYSTGAEOLFENKIGQVDFEINNEIRDPSSKALIRKYTTEADDL	420
Dp	361	DFINNEIRDPSSKALIRKYSTGAEOLFENKIGQVDFEINNEIRDPSSKALIRKYTTEADDL	420
Oy	421	FENKIGQTVDFINKEIRDPSSKALIRKYSTADNDLLEK	458
Dp	421	FENKIGQTVDFINKEIRDPSSKALIRKYSTADNDLLEK	458

```

RESULT 2
ID Q9UA65 PRELIMINARY; PRT: 488 AA.
AC Q9UA65;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RHOPTRY-ASSOCIATED PROTEIN 1.
CN RAP-1.
OS Babesia caballi.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxId:5871;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-USDA;
RX MEDLINE=98294770; PubMed=1036459;
RA Kappmeyer L.S., Perryman L.E., Hines S.A., Bassler T.V., Katz J.B.,
RA Hennager S.G., Knowles D.P.;
RT "Detection of equine antibodies to babesia caballi by recombinant B.
RT caballi rhoptry-associated protein 1 in a competitive-inhibition
RT enzyme-linked immunosorbent assay";
RL J. Clin. Microbiol. 37:2285-2290(1999).
DR EMBL; AF092736; AAD0081.1;
DR InterPro; IPR004318; RAP-1.
DR Pfam; PF03085; RAP-1;
DO SEQUENCE 488 AA; 55194 MW; 08EDA252D16DC77E CRC64;

```

Query Match	99.88	Score 2355	DB 5	Length 488
Best Local Similarity	99.88	Pred. No. 2.6e-147		
Matches 457	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

OY	1	MAPSVDVKTLLLAASESDSANMYMISDKSDYLNAVNDNFARICSOVPKSGNC	60
Dd	31	MAPSDSVGDVTKTLAASESDSANMYMISDMSDYLSAVSDFARICSOVPKSGNC	90
OY	61	ASVASVMRCACKODCLTQSLAKYPELEAKYOPTLPDPYOLEAMFLEPKESDANPANSTEK	120
Dd	91	ASVASVMRCACKOCCLTQSLAKYPELEAKYOPLTPDPYOLEAMFLEPKESDANPANSTEK	150
OY	121	RFWWFERRGKNHSHFYHDLVFNLLKEKNVTRDADATDIENFASTRLYMATLTYKYTVNDEF	180
Dd	151	RFWWMFRGRGKNHSHFYHDLVFNLLKEKNVTRDADATDIENFASTRLYMATLTYKYTVNDEF	210
OY	181	GASFPNKUSFTTTGLFGWGIRKALKOIIIRSNL?LDIGTBHSYSRLOHTTSXKOYMOOTIP	240
Dd	211	GASFPNKUSFTTTGLFGWGIRKALKOIIIRSNL?LDIGTBHSYSRLOHTTSXKOYMDIOIP	270

OY	261	ALPFAKRESLVORLLATVAGVDDPWYKKWMTKKNVNVNF1PTKKFENKEIREP	3000
Db	271	ALPFAKRESLVYVORLLATVAGVDDPWYKKWMTKKNVNVNF1PTKKFENKEIREP	3300
OY	301	SKALKEKYSTDTKDLFENKIGÖTVDFENKEIRDPSSKALKEKYSNDAKDLFENKIGÖTV	3600
Db	331	SKALKEKYSTDTKDLFENKIGÖTVDFENKEIRDPSSKALKEKYSNDAKDLFENKIGÖTV	3900
OY	361	DFINNEIRDPSSKALIRKYSTAEDL FENKIGÖTVDFINNEIRDPSSKALIRKYTEADL	4200
Db	391	DFINNEIRDPSSKALIRKYSTAEDL FENKIGÖTVDFINNEIRDPGKALIRKYTEADL	4500
OY	421	FENKIGÖTVDFINKEIRDPSSKALIRKYTEADNULLEK	458
Db	451	FENKIGÖTVDFINKEIRDPSSKALIRKYTEADNULLEK	488

```

RESULT 3
O9TVG3
ID O9TVG3 PRELIMINARY; PRT; 565 AA.
AC O9TVG3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN-1.
GN RAP-1.
OS Babesia bovis.
OC Eukaryota, Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5865;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UR, AND CG-P.
RA Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
RT "Structure, sequence, and transcriptional analysis of the Babesia
RT bovis rap-1 multigene locus."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030058; AAB84270.1; -.
DR InterPro; IPR004318; RAP-1.
DR Pfam; PF03085; RAP-1; 1.
SQ SEQUENCE 565 AA; 64933 MW; F5D769DAE92CDA3F CRC64;

```

Query Match	35.28;	Score 831.5;	DB 5;	Length 565;
Best Local Similarity	35.78;	Pred. No. 6.5e+47;		
Matches 179; Conservative	80;	Mismatches 193;	Indels 49;	Gaps 6;

[illegible]

GN RAP-1.
 OS Babesia bovis.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
 OX NCBI_TaxID=5865;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MEXICO MO7;
 RX MEDLINE=98327208; PubMed=9662706;
 RA Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
 RT "Structure, sequence, and transcriptional analysis of the Babesia
 RT bovis rap-1 multigene locus."
 RL Mol. Biochem. Parasitol. 93:215-224(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T2B, AND RIA;
 RA Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
 RT "Structure, sequence, and transcriptional analysis of the Babesia
 RT bovis rap-1 multigene locus."
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF021149; AAC27387.1; -
 DR EMBL: AF030054; AAB84264.1; -
 DR EMBL: AF030055; AAB84265.1; -
 DR EMBL: AF030059; AAB84269.1; -
 DR EMBL: AF027149; AAC27386.1; -
 DR InterPro: IPR004318; RAP-1.
 DR Pfam: PF03085; RAP-1; 1.
 SQ SEQUENCE 565 AA; 64933 MW; 6AC555E3B6F55615 CRC64;

Query Match 35.0%; Score 826.5; DB 5; Length 565;
 Best Local Similarity 35.5%; Pred. No. 1,4e-46;
 Matches 178; Conservative 79; Mismatches 195; Indels 49; Gaps 6;

QY 1 MAPSDSGDVTYTLTLLAASSVDSANAYMINSDMSDYLAVSDNFAERICQVPGKSGNS 60
 DB 31 LAPAEVVGDLSTLEFADTLMTLRDHMHNTKMKHVLSNGRQIYNDVCSNAPEDSNCR 90
 QY 61 ASVSANMSCAKQDCITLSTLKYPLAKYQPLTLPDPOYLEAFILFKESDANPANSTER 120
 DB 91 EYVNNYADRCENYGCFTIDNVKRYLOEYQPLSPNPYOLDAAFRLFKESASNPANNSYK 150
 QY 121 RFMRFRRCGNHNSYFHDVFNLEKAVTRDADATDIENFASRYLVATLYKTYTNVDER 180
 DB 151 REMPLRRNGANHGDYHFTYGLNNVYHEGTTDVEYLVNKLYMATNMYKTYLVNSM 210
 QY 181 GASFFNKLSTTGLFGWGIRALKQIIRSNLPDICTEHSVSRLOHTSSYKDYMDTOIP 240
 DB 211 NAKFFNRFSFTTKIFSRIRQLTSDIIRNVPEDF-EERSIERITQLTSSYEDYMLTOIP 269
 QY 241 ALPKFARRSLVAVQRLATVAGYVDTPLYKKYMKLKNFVNRVFTPIPKF----- 292
 DB 270 TLSKFAIRYADVKKVLLGSLTSYVEAPYKRWIKKFRDFFSKNVQPTKKFIEDTNEYA 329
 QY 293 -----FNKEIRREPSKALKEKYSTDPKDLFENKIGOGTVD 326
 DB 330 KNYLKANVAEPTKKKMODTHEKTKGLKEVNAEPTTFKEAPQVTKHFFEDENIGOPTKE 389
 QY 327 FENKEIRDSKALKKEKVSNDADLFENKIGOGTVDFINNEIRDSKALIRKYSTGAEDLF 386
 DB 390 FFEAPQATKHFHLDENIGOPTKEFF-REAPQATKHFHLDENIGOPTKEFFRDVQVYKVI 448
 QY 387 ENKIGOGTVDF-----INNEIRDSKALIRKYSTGAEDLFENKIGOGTVDFIN 435
 DB 449 TENIAOPTKEFFREVPYHATMKVLNENIAOPAKEIIHEFGTGAKN-FISAHEGTOFLNE 507
 QY 436 EIRDSKALIR-KVSTEADNL 455
 DB 508 TVGQPTKEFLNGALETTKDAL 528

RESULT 7
 ID 017115 PRELIMINARY; PRT: 565 AA.
 AC 017115;

DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MEROZOITE SURFACE PROTEIN.
 GN BV60.
 OS Babesia bovis.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
 OX NCBI_TaxID=5865;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MO7; TISSUE=LAMBDA-ZAP II LAMBDA-G711;
 RX MEDLINE=91304520; PubMed=1712911;
 RA Suarez C.E., Palmer G.H., Jasmer D.P., Hines S.A., Perryman L.E.,
 RA McElwain T.F.;
 RT "Characterization of the gene encoding a 60-kilodalton Babesia bovis
 RT merozoite protein with conserved and surface exposed epitopes."
 RL Mol. Biochem. Parasitol. 46:45-52(1991).
 DR EMBL: M38218; AAA62695.1; -
 DR InterPro: IPR004318; RAP-1.
 DR Pfam: PF03085; RAP-1; 1.
 SQ SEQUENCE 565 AA; 64976 MW; B77D347DCE12C874 CRC64;

Query Match 35.0%; Score 826.5; DB 5; Length 565;
 Best Local Similarity 35.5%; Pred. No. 1,4e-46;
 Matches 178; Conservative 79; Mismatches 195; Indels 49; Gaps 6;

QY 1 MAPSDSGDVTYTLTLLAASSVDSANAYMINSDMSDYLAVSDNFAERICQVPGKSGNS 60
 DB 31 LAPAEVVGDLSTLEFADTLMTLRDHMHNTKMKHVLSNGRQIYNDVCSNAPEDSNCR 90
 QY 61 ASVSANMSCAKQDCITLSTLKYPLAKYQPLTLPDPOYLEAFILFKESDANPANSTER 120
 DB 91 EYVNNYADRCENYGCFTIDNVKRYLOEYQPLSPNPYOLDAAFRLFKESASNPANNSYK 150
 QY 121 RFMRFRRCGNHNSYFHDVFNLEKAVTRDADATDIENFASRYLVATLYKTYTNVDER 180
 DB 151 REMPLRRNGANHGDYHFTYGLNNVYHEGTTDVEYLVNKLYMATNMYKTYLVNSM 210
 QY 181 GASFFNKLSTTGLFGWGIRALKQIIRSNLPDICTEHSVSRLOHTSSYKDYMDTOIP 240
 DB 211 NAKFFNRFSFTTKIFSRIRQLTSDIIRNVPEDF-EERSIERITQLTSSYEDYMLTOIP 269
 QY 241 ALPKFARRSLVAVQRLATVAGYVDTPLYKKYMKLKNFVNRVFTPIPKF----- 292
 DB 270 TLSKFAIRYADVKKVLLGSLTSYVEAPYKRWIKKFRDFFSKNVQPTKKFIEDTNEYA 329
 QY 293 -----FNKEIRREPSKALKEKYSTDPKDLFENKIGOGTVD 326
 DB 330 KNYLKANVAEPTKKKMODTHEKTKGLKEVNAEPTTFKEAPQVTKHFFEDENIGOPTKE 389
 QY 327 FENKEIRDSKALKKEKVSNDADLFENKIGOGTVDFINNEIRDSKALIRKYSTGAEDLF 386
 DB 390 FFEAPQATKHFHLDENIGOPTKEFF-REAPQATKHFHLDENIGOPTKEFFRDVQVYKVI 448
 QY 387 ENKIGOGTVDF-----INNEIRDSKALIRKYSTGAEDLFENKIGOGTVDFIN 435
 DB 449 TENIAOPTKEFFREVPYHATMKVLNENIAOPAKEIIHEFGTGAKN-FISAHEGTOFLNE 507
 QY 436 EIRDSKALIR-KVSTEADNL 455
 DB 508 TVGQPTKEFLNGALETTKDAL 528

RESULT 8
 ID 090008 PRELIMINARY; PRT: 565 AA.
 AC 090008;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE RHOPTRY ASSOCIATED PROTEIN-1.
 GN RAP-1.
 OS Babesia bovis.


```

Matches 178; Conservative 80; Mismatches 194; Indels 49; Gaps 6;

Oy 1 MAPSDVSDVDTKTLAASESDVSAANAYMNSDMDYLSAVSDNFAERCSQVPGKSNCS 60
    ::::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 31 LAPAVVDLDTSTLEADTLMTLRDHMHNTIKDKMHVLSNGREQIVNDVCSNAPDSNCR 90
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 61 ASVASYMRCARACODLTLOSLKPYLEAKYQPTLRDPQVLEAFILFKESDANPNANSTFK 120
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 91 EVVNNYADRCBCEYCGFTIDNKYPLTXQEQPSTLPNPQLDAFRLFKESASNPAPKNSVK 150
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 121 RFWMRFRRGKNHSYFHDVLVFNLEKNVTRDADATDIENFASRLYMATLYTKTYTNVDEF 180
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 151 REMLFRFGANGHGDHYFYATGGLNNNVHVEEGTQDVEYLVNVLVMATMYNTYTLTVNSM 210
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 181 GASEFNKTSFTTGFGWGKIRALKOILISNPLDGTGHSVSRLOHTISSYDYMDYTOIP 240
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 211 NAKFENRFSPTTKTIRSRKQPTLSDIRNNVEDP--EESISERTITQULTSSYEDYMLTOIP 269
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 241 ALPKPAKFFSLVAVORLLATVAGYVDTPWPKWKMYKLNKNVNRVFIPTKPF----- 292
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 270 TLSKARARYADWKKVVLGSLSYVEAEPMYKWKIKKFRDFESKNTQPTKKTIEDTNEVT 329
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 293 -----FNKEIPEPSKALKEKYSTDTKDLFEKKIGOGTYD 326
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 330 KNYLKANAAPETPKKEMODTHEKTKGYLKENVAEPTKTFEKAPQVTKHFFEDNTGQPTKE 389
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 337 FPNKEIROPDSKALKEKVSNDAKDLFENKIGOGTYVFINNEIDPSKALIRKYSTGAEDLF 386
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 390 FPREAPQATKHRLDENIGQPTKEFF--REAPQATKHRLDENINQAPTKPEFKVDQVQTKKVI 448
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 387 ENKIGOGTYVD-----INNEIDPSKALIRKYVTEADDLFENKIGOGTYVDFTIK 435
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 449 TENIAQPTKEFLREVPHPATMKVLNNININQAPAKEIIHFEGTGAKN--FISAHGEGTKQFLNE 507
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 436 EIRDPSSKALIR-KVSTEADNLT 455
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 508 TYGQPTKEFLNGALETTTKDAL 528
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
O9U004 PRELIMINARY: PRT: 565 AA.
AC O9U004:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Db DE RHOPTRY ASSOCIATED PROTEIN-1.
GN RAP-1.
OS Babesia bovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
CX NCBI_TaxID=5665;
OX (1)
RP SEQUENCE FROM N.A.
RC STRAIN=RLA;
RA Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
RT "Structure, sequence, and transcriptional analysis of the Babesia
RT bovis rap-1 multigene locus."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030062; AAB84272.1; -.
DR InterPro; IPR004518; RAP-1.
DR Pfam; PF03085; RAP-1; 1.
SQ SEQUENCE 565 AA; 64979 MW; 7F5E0019DEBA1892 CRC64;

Query Match: 35.0%; Score 825.5; DB 5; Length 565;
Best Local Similarity 36.5%; Pred. No. 1.6e-46;
Matches 183; Conservative 77; Mismatches 192; Indels 49; Gaps 8;

Oy 1 MAPSDVGDVDTTLTAAASEVDASANAYMNSDMSDYLSAVSDNFAERICSQVPGKSNCS 60
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 31 LAPAVVGDGLSTLEADTLMTLRDHMHNTIKDKMHVLSNGREQIVNDVCSNAPDSNCR 90
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 61 ASVASYMRCARACODLTLOSLKPYLEAKYQPTLRDPQVLEAFILFKESDANPNANSTFK 120
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 91 EVVNNYADRCBCEYCGFTIDNKYPLTXQEQPSTLPNPQLDAFRLFKESASNPAPKNSVK 150
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 121 RFWMRFRRGKNHSYFHDVLVFNLEKNVTRDADATDIENFASRLYMATLYTKTYTNVDEF 180
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 151 REMLFRFGANGHGDHYFYATGGLNNNVHVEEGTQDVEYLVNVLVMATMYNTYTLTVNSM 210
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 181 GASEFNKTSFTTGFGWGKIRALKOILISNPLDGTGHSVSRLOHTISSYDYMDYTOIP 240
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 211 NAKFENRFSPTTKTIRSRKQPTLSDIRNNVEDP--EESISERTITQULTSSYEDYMLTOIP 269
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 241 ALPKPAKFFSLVAVORLLATVAGYVDTPWPKWKMYKLNKNVNRVFIPTKPF----- 292
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 270 TLSKARARYADWKKVVLGSLSYVEAEPMYKWKIKKFRDFESKNTQPTKKTIEDTNEVT 329
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 293 -----FNKEIPEPSKALKEKYSTDTKDLFEKKIGOGTYD 326
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 330 KNYLKANAAPETPKKEMODTHEKTKGYLKENVAEPTKTFEKAPQVTKHFFEDNTGQPTKE 389
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 337 FPNKEIROPDSKALKEKVSNDAKDLFENKIGOGTYVFINNEIDPSKALIRKYSTGAEDLF 386
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 390 FPREAPQATKHRLDENIGQPTKEFF--REAPQATKHRLDENINQAPTKPEFKVDQVQTKKVI 448
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 387 ENKIGOGTYVD-----INNEIDPSKALIRKYVTEADDLFENKIGOGTYVDFTIK 435
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 449 TENIAQPTKEFLREVPHPATMKVLNNININQAPAKEIIHFEGTGAKN--FISAHGEGTKQFLNE 507
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 436 EIRDPSSKALIR-KVSTEADNLT 455
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 508 TYGQPTKEFLNGALETTTKDAL 528
    ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|


```

D6		91	EVNNVNYADRCMEYCGFTIDNKKYPLDYOEYDLSLPNPQDLAAFRLEKESASNPAAKSXVK	150
QY	121	RFWMRFRGKGHSHFPHDIYENLLEKNNTROADDATIEDFAFSRYLYMATLYKKTYNDEF	180	
D6	151	REWRFRFGANHG DYHFVVTGLNNNVHGGEGTDVEVLVKKLVLMAMWMTKTYLTIVNSM	210	
OY	181	GASEFNKSTFTGTGEWGIKRALKOILRSNPLDIGTEHSYSRLQHTTSYKYDMYTQIP	240	
D6	211	NAKFNRNRSFTTKIFSRIIRDTLDIIIMVNYPDFE-EERSIERITQTOLSSVEDYMLTQIP	269	
QY	241	ALPKFAKRESLNVVQRLLATVAGVDIPIWKYKWTMKLKLENVANKRYFIPTKAF-----	292	
D6	270	TLSFEARFYADMVKKVLLGSITSYEAPWMYRWIKKPFEDFSKKNVTOPTKKEFIEDTNEVT	329	
QY	293	---FNKEIREDSKA-----LKEKSTDPKDLFEKKIGGYTVDFPNKEIRDPSK	337	
D6	330	KNYLKANAAYETTKFMDEMDTHEKTKGYLKENVAEEPKTFEK-ELAQYVTHFFDENICGPTK	388	
QY	338	ALKEKVSNDARDLFENKIGGYTVDF-----FINNEIRDPSKALIRKYSTGAEDLF	386	
D6	389	EERFRAPOQATHFLFDENICGPTKEFEREAROVTKHFLFDENTIAQPTKEFFRDVPQVTKKVI	448	
QY	387	ENKIGGCVDF-----INNEIRDPSKALIRKYTTBADLFEKKIGGYTVDFENK	435	
D6	449	TENIAQPKEKLEKEYPHTTMKVLENENIAOPAKKEIHFGTGAKN-FISAHEGTRKOFNE	507	
QY	436	EIRDPSKALIR-KVSTEADNL	455	
D6	508	TVGOPTKEFLNGALETTKDAL	528	
 RESULT 12 Q17126 PRELIMINARY; PRT; 456 AA.				
ID	017126			
AC	017126:			
DT	01-NOV-1996 (TREMBLrel_01, Created)			
DT	01-NOV-1996 (TREMBLrel_01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel_19, Last annotation update)			
DE	RHOPTPR PROTEIN.			
OS	Babesia canis.			
OC	Eukaryota; Alveolata; Apicomplexa; Epioplasmda; Babesiidae; Babesia.			
OX	NCBI_Taxid=5867;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-TOMNSVILLE.			
RX	MEDLINE-93165069; PubMed-8433711.			
RA	Dalrymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R., Wright I.G.;			
RT	"Characterisation of a family of multi-copy genes encoding rhoptry protein homologues in Babesia bovis, Babesia ovis and Babesia canis."			
RL	Mol. Biochem. Parasitol., 57:181-192(1993).			
DR	EMBL; M91168; AAA27807.1; -			
DR	InterPro; IPRO01064; CrystalLin.			
DR	InterPro; IPRO04318; RAP-1.			
Pfam:	PF003085; RAP-1; 1.			
DR	PROSITE; PS00225; CRYSFALLIN_BETAGAMMA; UNKNOWN_1.			
SQ	SEQUENCE 456 AA; 52470 MM; 87C57CA0A0ADB924 CRC64;			
 Query Match 32.7%; Score 770.5; DB:5; Length 456; Best Local Similarity 35.0%; Pred.No.5.le-43; Matches 161; Conservative 95; Mismatches 161; Indels 43; Gaps 9;				
OY	1	MAPSDVGDYVTKTLTAASESVDASAANAAYINSMSDYLAAASDNFAERICQVPGKSNCS	60	
D6	31	LKSGAGARKTSLTLNVDASTRALLEGVRMAAANAENGNGREEBEAEVANGINAETTCQ	90	
OY	61	ASVASVMSRCAKODCLTQLSUKYPLEAKYQPLTPDPLQLEAAFLFKESDANPANSTEK	120	
D6	91	KSAVEYVESCVRYDCFSIENOKYPOEKKEYQPLTPNPQLEAAFYVFNNSSNPNTKPTE	150	
QY	121	RFWMRFRGKGHSHFPHDIYENLLEKNNTROADDATIEDFAFSRYLYMATLYKKTYNDEF	180	
D6	151	AFWMFERRGRGAHNFLVNLTKNLSDSMNVDVLEGFVRRYATAWMATYTKITTALDVY	210	

Qy	101	GASFNKLSFTTGGJGSGIKRALKOIRSLNPLDIGHESVHSLQHTTSYKXUOTPOIP	240
Db	211	NARINKIAFSRHLFGKOIRKALNIIIRSNIPDEFG-KIVNDRIRRHMGCEETMMKQVP	269
Qy	241	ALPFKARFSLMNVQRLLATVAGIVDTPWVKKKWYMKLKNPMVNRVETPTKPFENKEIRBP	300
Db	270	SLPFAKKYAGMVAWKSILKNNGAVQROPMFKKLNQOIRNPFVANKIHEPTKEEFVANKIHER	329
Qy	301	SKALKEKVSIDTRKLPFNKIGQGVDFPFNKEIRDPKALKEKYSNDAKDLFENKIGQGV	360
Db	330	-----TKKEFVANKIHEPTKEEFVANKIHEPT-----KEEFVANKIHEPTK	367
Qy	361	DFINNEIRDEPSKALIRKYSTGAEDLFENKIGQGVDFINNEIRDPKALIRKYTEADDL	420
Db	368	EEFVANKIHEPTKEEFVNMVPGAFQKISEKKGR-----HLMS-SKTYVPE--DEPSSS	416
Qy	421	FENKI---GQGVTF-DFINKEIRDP-----SKALIRKYSTE	451
Db	417	LENFAVEDGQLTGMGDVDFEFAKPTQYEDGSGSESLNIEVGNL	456

RESULT 13		
ID	017256	
AC	017256	PRELIMINARY; PRT; 496 AA.
DT	01-NOV-1996	(TREMBLrel. 01, Created)
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)
DE	ROPTRY PROTEIN.	
OS	Babesia ovis.	
OC	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.	
NCBI_taxid=5869;		

RC STRAIN=ANKARA;
RX MEDLINE=93165069; PubMed=8433711;
RA Dairymple B., Casu R.E, Peters J.M., Dimmock C., Gale K.R, Bose R.,
RA Wright I.G.;
RT *Characterisation of a family of multi-copy genes encoding rhotptry
RT protein homologues in Babesia bovis, Babesia ovis and Babesia canis."
RL Mol. Biochem. Parasitol. 57:181-192(1993).
DR EMBL; M91169; AAAZ7805.1; -
DR InterPro; IPR004318; RAP-1.
DR Pfam; PFO3085; RAP-1; 1.
SQ SEQUENCE 496 AA; 56892 MW; 2E4020EBD2AF499 CRC64;

Query Match	32.2%;	Score 759.5;	DB 5;	Length 496;
Best Local Similarity	34.3%;	Pred. No. 3e-42;		
Matches 161; Conservative	93;	Mismatches 173;	Indels 43;	Gaps

[illegible]

Db	330	DTPNNTKDALCPRLDPAVEENIVPSPDYLRRKONISQSNYNQNHKIDSLTEPKRPH	389
Qy	340	KEVSNDAKLFENKIGGQVDFINNEIDRPSKLLIKRVSTGADLFENKIGQGVFIN	399
Db	390	IGIAANHARQYIDDKVKN-----AKELVSAAKRARGIVADHYKPPALSDITN	433
Qy	400	---NEIDRPSKALLIKRV---TEADDLFENKIGGQVDFINKEIRDRPSKA	443
Db	437	VKKMDLDAVN--IRNIRGSSQDDNNQDETEEEKVEEVPFELKQKEYA	484

RESULT	14
ID	Q17121
AC	Q17121; PRELIMINARY;
DT	01-NOV-1996 (TREMBLrel_01, Created)
DT	01-NOV-1996 (TREMBLrel_01, Last sequence update)
DT	01-DEC-2001 (TREMBLrel_19, Last annotation update)
DE	RHOPTRY ASSOCIATED PROTEIN 1 (FRAGMENT).
	RHOPTRY
	445 AA.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia
OX NCBI_TaxId:5865;
RN [1]
RP
RT SEQUENCE FROM N.A.
RC SPRAIN-MO7;
RA Snares C.E., Palmer G.H., Hines S.A., McElwain T.F.;
RT "The Babesia bovis rhoptry-associated protein-1 intergenic region
RT encodes a functional eukaryotic promoter.",
RD submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.

DR INTERPIO; 1FR04318; RAP-1.
DR Pfam; PF03085; RAP-1; 1.
FT NON_TER 1 1
SQ SEQUENCE 445 AA; 5135 MW; 3A324715F8DAFB7C CRC64;

[illegible]

ID	Q17257	PRELIMINARY:	PRT:	321 AA.
DB	121	VEDEF-EERSTERITOLTSIEDMLTIOPTLSKFAKRYADMKVLLGSLSTVEAPWY	178	
QY	271	KRWYMLKLNFMVNRVFIPTKF-----FNKE	296	
DB	180	KRWIKKFPDEFPSKNVGTQTKKEIEDTNEVTKNYLKANVAEPTKKFMOQTHEKTGYLKEN	239	
QY	297	IRPSKALKKGVSTDTKOLFENKIGQGVDFENKEIRDPKALKKGVNDKADLFENKIG	350	
DB	240	VAEPKTFEKKAPOVYTKHEFDENIGOPTKEFFREAPQATKHFLENIGOPTKEFF-REAP	296	
QY	357	OGTVDFINNEIRDSKALIRKYSTGAEDLFENKIGQGVDF-----INNEIRDP	406	
DB	299	QATKHFLEGENIAOPTKEFFKVDPOVYTKVITENIAOPTKEFLREVPATKVLNENIAOP	356	
QY	406	SKALIRKYTTAADDLFENKIGQGVDFINKEIRDSKALIR-KYSTEDNL	455	
DB	359	AKETIHGEGTAKN-FISAHBEGRKOFLENTGVGOPTKEFLGALETTKDAL	408	

Query Match 26.8%; Score 632.5; DB 5; Length 321;
Best Local Similarity 47.2%; Pred. No. 4e-34;
Matches 133; Conservative 45; Mismatches 87; Indels 17; Gaps 6;

OC 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE (60.2 OR .3) RHOPTRY PROTEIN (FRAGMENT).
OS Babesia ovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
ON NCBI_TaxID=9869;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANKARA;
RX MEDLINE=93165069; PubMed=8433711;
RA Dairymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R., Wright I.G.;
RT "Characterisation of a family of multi-copy genes encoding rhoptry protein homologues in Babesia bovis, Babesia ovis and Babesia canis.",
RL Mol. Biochem. Parasitol. 57:181-192(1993).
DR EMBL: M91173; AAA27811.1; -
DR InterPro: IPR004318; RAP-1.
DR Pfam: PF03085; RAP-1; 1.
FT NON_TER 1
SQ SEQUENCE 321 AA; 37469 MW; 0BFCBE13813D1108 CRC64;

Query Match 26.8%; Score 632.5; DB 5; Length 321;
Best Local Similarity 47.2%; Pred. No. 4e-34;
Matches 133; Conservative 45; Mismatches 87; Indels 17; Gaps 6;

OC 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RHOPTRY PROTEIN (FRAGMENT).
OS Babesia ovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
ON NCBI_TaxID=9869;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANKARA;
RX MEDLINE=93165069; PubMed=8433711;
RA Dairymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R., Wright I.G.;
RT "Characterisation of a family of multi-copy genes encoding rhoptry protein homologues in Babesia bovis, Babesia ovis and Babesia canis.",
RL Mol. Biochem. Parasitol. 57:181-192(1993).
DR EMBL: M91173; AAA27811.1; -
DR InterPro: IPR004318; RAP-1.
DR Pfam: PF03085; RAP-1; 1.
FT NON_TER 1
SQ SEQUENCE 273 AA; 31779 MW; BE954830D9EAC399 CRC64;

Query Match 24.3%; Score 574; DB 5; Length 273;
Best Local Similarity 43.3%; Pred. No. 2.3e-30;
Matches 127; Conservative 41; Mismatches 73; Indels 52; Gaps 7;

OC 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN PRECURSOR.
OS Babesia divergens.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
ON NCBI_TaxID=32595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DRUMANESS;
RX MEDLINE=96379225; PubMed=8784776;
RA Skuce P.J., Mallon T.R., Taylor S.M.;
RT "Molecular cloning of the rhoptry associated protein homologue of Babesia divergens".
RL Mol. Biochem. Parasitol. 77:99-102(1996).
DR EMBL: Z49818; CA88970.1; -
DR InterPro: IPR004318; RAP-1.
DR Pfam: PF03085; RAP-1; 1.
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 408
FT SEQUENCE 408 AA; 46133 MW; E74440D6F5C1D151 CRC64;

Query Match 24.1%; Score 569.5; DB 5; Length 408;
Best Local Similarity 36.8%; Pred. No. 7.6e-30;
Matches 125; Conservative 59; Mismatches 137; Indels 19; Gaps 6;

OC 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN.
OS Babesia ovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
ON NCBI_TaxID=9869;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANKARA;
RX MEDLINE=93165069; PubMed=8433711;
RA Dairymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R., Wright I.G.;
RT "Characterisation of a family of multi-copy genes encoding rhoptry protein homologues in Babesia bovis, Babesia ovis and Babesia canis.",
RL Mol. Biochem. Parasitol. 57:181-192(1993).
DR EMBL: M91173; AAA27811.1; -
DR InterPro: IPR004318; RAP-1.
DR Pfam: PF03085; RAP-1; 1.
FT NON_TER 1
SQ SEQUENCE 273 AA; 31779 MW; BE954830D9EAC399 CRC64;

Query Match 24.3%; Score 574; DB 5; Length 273;
Best Local Similarity 43.3%; Pred. No. 2.3e-30;
Matches 127; Conservative 41; Mismatches 73; Indels 52; Gaps 7;

OC 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN PRECURSOR.
OS Babesia divergens.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
ON NCBI_TaxID=32595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DRUMANESS;
RX MEDLINE=96379225; PubMed=8784776;
RA Skuce P.J., Mallon T.R., Taylor S.M.;
RT "Molecular cloning of the rhoptry associated protein homologue of Babesia divergens".
RL Mol. Biochem. Parasitol. 77:99-102(1996).
DR EMBL: Z49818; CA88970.1; -
DR InterPro: IPR004318; RAP-1.
DR Pfam: PF03085; RAP-1; 1.
KW Signal.
FT SIGNAL 1 21
FT CHAIN 22 408
FT SEQUENCE 408 AA; 46133 MW; E74440D6F5C1D151 CRC64;

Query Match 24.1%; Score 569.5; DB 5; Length 408;
Best Local Similarity 36.8%; Pred. No. 7.6e-30;
Matches 125; Conservative 59; Mismatches 137; Indels 19; Gaps 6;

OC 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN.
OS Babesia ovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
ON NCBI_TaxID=9869;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANKARA;
RX MEDLINE=93165069; PubMed=8433711;
RA Dairymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R., Wright I.G.;
RT "Characterisation of a family of multi-copy genes encoding rhoptry protein homologues in Babesia bovis, Babesia ovis and Babesia canis.",
RL Mol. Biochem. Parasitol. 57:181-192(1993).
DR EMBL: M91173; AAA27811.1; -
DR InterPro: IPR004318; RAP-1.
DR Pfam: PF03085; RAP-1; 1.
FT NON_TER 1
SQ SEQUENCE 273 AA; 31779 MW; BE954830D9EAC399 CRC64;

Db 270 YMPAFSTFRFNWVDTLHKIKGYOKMPYKKMFNSVADFFKNSIGCKIKLNFSK--RAP 327
OY 301 SK-----ALKEKYSTDTKDLFENKIKGCTVDFPNKEIRDPSS 336
Db 328 SSSTEGAMHKVSHSVKMKMLNEKI-PVVKNFPEKDIRKSS 366

RESULT 18

015767 ID 015767 PRELIMINARY; PRT; 510 AA.
AC 015767;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RAP-1C.
GN RAP-1C.
OS Babesia bigemina.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5866;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MEXICO JG-29;
RA Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT "Genomic cloning of Babesia bigemina rap-1c gene."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026272; AAB82596.1;
DR InterPro; IPR004318; RAP-1.
DR Pfam; PF03085; RAP-1; 1.
SQ SEQUENCE 510 AA; 57468 MW; BAE9BDCF30C7EB06 CRC64;

Query Match 23.5%; Score 555; DB 5; Length 510;
Best Local Similarity 28.7%; Pred. No. 9.2e-29;
Matches 147; Conservative 80; Mismatches 177; Indels 108; Gaps 15;

OY 1 MAPS-----DSYGVDTKTLTLLAASESYDSANAYMINSMSDYLSAVSDNFAERICSOV 53
Db 31 MAPDHTFPAVDYDDDTKOLLESEQIEKA-----MGEELGLNDSIAEMCLGS 81
OY 54 PKGNSCSVSANVSRCAKODCLTQSLKYPLEAKYQPLTLPDPYOLEAFLTFRESAN 113
Db 82 KDEHCAIOAIYAVRCKEGECITDAVGKPKAKYKOLVLPDPYOLAFAFLFKNCRN 141
OY 114 PANSEKRFMRFRGRKNSYFHDVFNLEKNVTRDADATDIENFASRYLTMALYYKT 173
Db 142 ESRHMDFFMRFKGRYAAVYSESLNLRNLFGLGDKNALHGFVQKYFTMTAIYKT 201
OY 174 YTNVEFGASFENKLSFTTGLFGMGIKRALKOIRSNLPIDIGTEHSYRLOHITSYKD 233
Db 202 YLSLDATNAKIFNKIALAKHILGPKIKALKRIVKANPSPAL-QANDYKAIRPLAYGRQ 260
OY 234 YMDQIAPLPFAKRFSLMAYVQRLATVAGYVDPYKRWYKMLKNFVNRYEIPTRKEF 293
Db 261 YMASQIPSLPFPAVYKFSMVYALVDNLTVGQCPWYKRWKFCVNLFTGKQ--PSEKAY 318
OY 294 NKEIREPSKALKKYSTTKOLFENKIKGCTVDFPNKEIRDPSSKALKKESV----- 345
Db 319 --EIDEPATEEE-----TEPEENK-----SVFGK-----VKELGIRIRENTGIF 357
OY 346 ---DAK-----DLPENKIGCTVDFPINNEIRDPSSKALIR 376
Db 358 RKGEAKTSHLSSEEDINGSLSSADALLEPVLVME-KEGEAQ-----NEAGEPEVAAP 412
OY 377 KVS-----TGADLPENKIGQ-----GTVDFINNEIRD-----PSKALI 410
Db 413 KAPESENGELADQYVGAGTAVSTAGEEESLEAPKGTODLMHEDEQEPSEDELPAKRR 472
OY 411 RKVYTEADLPENKIGCTVDFPINKEIRDPSSK 442
Db 473 KASSTGYKKFFKNILDTGAIKDAASRIGRPKK 504

RESULT 19

O9TVNO ID O9TVNO PRELIMINARY; PRT; 191 AA.
AC O9TVNO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RAP-1 BETA (FRAGMENT).
GN RAP-1.
OS Babesia bigemina.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5866;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98135662; PubMed=9476795;
RA Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT "Genetic variation in the dimorphic regions of rap-1 genes and rap-1 loci of Babesia bigemina."
RT Mol. Biochem. Parasitol. 90:479-483(1997).
RL EMBL; AF014768; AAC47870.2;
DR EMBL; AF014757; AAC47859.2;
DR EMBL; AF014758; AAC47860.2;
DR EMBL; AF014760; AAC47862.2;
DR EMBL; AF014762; AAC47864.2;
DR InterPro; IPR004318; RAP-1.
DR Pfam; PF03085; RAP-1; 1.
FT NON_TER 1
FT NON_TER 191
SQ SEQUENCE 191 AA; 21574 MW; B66D7416F59CA263 CRC64;

Query Match 22.6%; Score 532; DB 5; Length 191;
Best Local Similarity 52.8%; Pred. No. 8.4e-28;
Matches 103; Conservative 32; Mismatches 52; Indels 8; Gaps 2;

OY 4 SDSGVDTKTLTLLAASESYDSANAYMINSMSDYLSAVSDNFAERICSOVPRKNSCSASV 63
Db 5 AEVGDVSKTLLLEANEVNAEMEAQVKNMQSQLSNVKEITVGEYCEKVAAGNSTCGESV 64
OY 64 SAYMRCRCAKODCLTQSLKYPLEAKYQPLTLPDPYOLEAFLTFRESANPANSTEKRW 123
Db 65 IAYVNRCEGDCDLTLTDSM-----RYKPLSLPNPYQOLAFAFLFRESNPNKNEVKRW 118
OY 124 MFRGRKNSYFHDVFNLEKNVTRDADATDIENFASRYLTMALYYKTYTNVDEFGAS 183
Db 119 MRSR--SSHGVDHNVVSLKKNVYRDPESNDVENFASQYFIYMTILYTYTLYTVPTAAK 176
OY 184 FENKLSFTTGLFGWG 198
Db 177 FENKLAFTTGLFGG 191

RESULT 20

018684 ID 018684 PRELIMINARY; PRT; 191 AA.
AC 018684;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RAP-1 BETA (FRAGMENT).
GN RAP-1.
OS Babesia bigemina.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5866;
RN [1]
RP SEQUENCE FROM N.A.
RA Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014767; AAC47869.2;
DR EMBL; AF014761; AAC47863.2;
DR InterPro; IPR004318; RAP-1.
DR Pfam; PF03085; RAP-1; 1.
FT NON_TER 1
FT NON_TER 191
SQ SEQUENCE 191 AA; 21622 MW; E666F1D5E9CB26F CRC64;

Matches 101; Conservative 32; Mismatches 54; Indels 8; Gaps 2;

OY 4 SSVSDYVTTTLAASVSASNAAYMINSDMDYLSAVSDNFAERKCSQYPKKSNCSASY 63
 DB 33 AAVVDVSTKTLAAENVEVAEMEAQINEDMKIQLANVETIYDEVCRCRDAGSPTRKSV 92
 OY 64 SAYMSRCAODCLTLOSLKYPEAKYQPLTPDPYOLEAFAILFKESDANPASTERKRF 123
 DB 93 IAYVDRCDGDCCLTLDMS-----KYKPLSLPPIYOLDLAFMLFRSDSPAKNEVKCFM 146
 OY 124 MFRFRKNHSYFHDLYFNLEKKNVTRDADATDIENFASRYLYMATLYKTYTNVDEFGAS 183
 DB 147 MMSR--SSSGDYHHFVYSLKLKNVADPSPNDVENFASQYFYMTLYKTYLTVDFTA 204
 OY 184 FPNKLSFTTGLFGWG 198
 DB 205 FPNKLAFTTRLFGFG 219

RESULT 24

OY 09UA66 PRELIMINARY; PRT; 95 AA.
 AC 09UA66;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE RHOTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
 GN RAP-1.
 OS Babesia caballi.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
 OX NCBI_TaxId=5871;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-USDA;
 RX MEDLINE=99294770; PubMed=10364599;
 RA Kappeyer L.S., Perryman L.E., Hines S.A., Baszler T.V., Katz J.B.,
 RT Hennager S.G., Knowles D.P.;
 RT "Detection of equine antibodies to babesia caballi by recombinant B.
 RT caballi rhoptry-associated protein 1 in a competitive-inhibition
 RT enzyme-linked immunosorbent assay.";
 RL J. Clin. Microbiol. 37:2285-2290(1999).
 DR EMBL; AF092735; AAD40980.1; -
 FT NON_TER 1
 SO SEQUENCE 95 AA; 10719 MW; 7714954ADBDB9FB CRC64;

Query Match 20.2%; Score 476; DB 5; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.7e-24;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 364 NNEIRNPSCALIRKYSTGADLFEKNIIGQGVDFINNEIRDPSCALIRKYTEADLFE 423
 DB 1 NNEIRNPSCALIRKYSTGADLFEKNIIGQGVDFINNEIRDPSCALIRKYTEADLFE 60
 OY 424 KIGOGTVDFINKEIRDPSCALIRKYSTGADLFE 458
 DB 61 KIGOGTVDFINKEIRDPSCALIRKYSTGADLFE 95

RESULT 25

OY 09GUD3 PRELIMINARY; PRT; 282 AA.
 AC 09GUD3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DE RAP1 BETA-3 (FRAGMENT).
 GN RAP-1 BETA-3.
 OS Babesia bigemina.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
 OX NCBI_TaxId=5866;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-UYA;

RX MEDLINE=98135662; PubMed=9476795;
 RA Hotzel T., Suarez C.E., McElwain T.F., Palmer G.H.;
 RT "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
 RT loci of Babesia bigemina.";
 RL Mol. Biochem. Parasitol. 90:479-489(1997).
 DR EMBL; AF017297; AAG14915.1; -
 FT NON_TER 1
 SO SEQUENCE 282 AA; 32549 MW; F537FA7947DE9BEE CRC64;

Query Match 18.8%; Score 442.5; DB 5; Length 282;
 Best Local Similarity 35.5%; Pred. No. 1.1e-21;
 Matches 105; Conservative 58; Mismatches 102; Indels 31; Gaps 11;

OY 159 FASRYLYMATLYKTYTNVDEFGASFPNKLSFTTGLFGKGIKRALKOIISNPLDGT 218
 DB 1 FASQYFMTLYKTYLTVDFTAKFPNKLAFTTRLFGFIOKALKLVSNLPLVDGT- 59
 OY 219 HVSRLQHTTSYKDYMDTQIPALPKFAKRFSLMVORLLATVAGYDTFMYKKWYMKL 278
 DB 60 HPEATTREIASGIGETMMTOVPAMTSFAERFSKMATYTLVYSDYHDLAYKRWYKFK 119
 OY 279 NFMVNRVFIPTKKEFNKEIREPSK-ALKEKYSTDTKDLFENKIGQGVDFENKEIRDP 337
 DB 120 EFTIVN-FETDPAKLIMKHVSQPVKTATYKLVPEHRQAIRNVGOSTKHIAN-GVRLAR 177
 OY 338 ALKEKSNDAKDLFENKI-----GQGVDFINNEIRDPSCALIRKYSTGADLFEKIG 391
 DB 178 MIKE---PSQOITREKLPHYLSKAKAGAVEHVVDYK--SKTRKRKSESSESYSD--- 228
 OY 392 QGVDFINNEIRDPSCALIRK-----YTAD----DLFENKIGQGVDFENKEIRD 439
 DB 229 -SEELIKESQYNPAKSAVASADKDYLVADWDALYK---YMWGQVGEIKD 280

RESULT 26

OY 09GUD4 PRELIMINARY; PRT; 282 AA.
 AC 09GUD4;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DE RAP1 BETA-3 (FRAGMENT).
 GN RAP-1 BETA-3.
 OS Babesia bigemina.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
 OX NCBI_TaxId=5866;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S2P;
 RX MEDLINE=98135662; PubMed=9476795;
 RA Hotzel T., Suarez C.E., McElwain T.F., Palmer G.H.;
 RT "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
 RT loci of Babesia bigemina.";
 RL Mol. Biochem. Parasitol. 90:479-489(1997).
 DR EMBL; AF017296; AAG14914.1; -
 FT NON_TER 1
 SO SEQUENCE 282 AA; 32549 MW; 7F9B1A7DA93B6BFI CRC64;

Query Match 18.7%; Score 441.5; DB 5; Length 282;
 Best Local Similarity 35.6%; Pred. No. 1.3e-21;
 Matches 104; Conservative 60; Mismatches 105; Indels 23; Gaps 9;

OY 159 FASRYLYMATLYKTYTNVDEFGASFPNKLSFTTGLFGKGIKRALKOIISNPLDGT 218
 DB 1 FASQYFMTLYKTYLTVDFTAKFPNKLAFTTRLFGFIOKALKLVSNLPLVDGT- 59
 OY 219 HVSRLQHTTSYKDYMDTQIPALPKFAKRFSLMVORLLATVAGYDTFMYKKWYMKL 278
 DB 60 HPEATTREIASGIGETMMTOVPAMTSFAERFSKMATYTLVYSDYHDLAYKRWYKFK 119
 OY 279 NFMVNRVFIPTKKEFNKEIREPSK-ALKEKYSTDTKDLFENKIGQGVDFENKEIRDP 337
 DB 120 EFTIVN-FETDPAKLIMKHVSQPVKTATYKLVPEHRQAIRNVGOSTKHIAN-GVRLAR 177

OY 338 ALKEKVSNDADLFENKI-----GQGTVDFINNEIRDPKALIRKYSTGAEDLFENKIG 391
178 MIKE-----PSQOIRREKLPYLSKAKGAVEHVVDKVK--SKTLKRAGESEESYSDDSE 231
OY 392 QGTVDFINNEIRDPKALIRKYSTGAEDLFENKIGQGTVDFINNEIRDPKALIRKYSTGAEDLFENKIG 439
232 EILKESQYNPAKSVASADKDEYLDYADMDALYKK--YMWVGVGVEIKD 280

RESULT 27

09GUD5 PRELIMINARY: PRT: 282 AA.
ID 09GUD5: PRT: 282 AA.

DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE RAP-1 BETA-3 (FRAGMENT).
OS Babesia bigemina.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBI_TaxID=5866;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CGA;
RX MEDLINE=98135662; PubMed=9476795;
RA Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT loci of Babesia bigemina.";
RL Mol. Biochem. Parasitol. 90:479-489(1997).
DR EMBL: AF017295; AAC14913.1; -.
FT NON_TER 1
SQ SEQUENCE 282 AA; 32549 MW; 14EB1A7CED7F7AA4 CRC64;

Query Match 18.7%; Score 440.5; DB 5; Length 282;
Best Local Similarity 35.5%; Pred. No. 1.5e-21;
Matches 105; Conservative 58; Mismatches 102; Indels 31; Gaps 11;

OY 159 FASRYLYMATLYKTYTYNVDGASFFNKLSFTTGLFGWGIRKALKQIIRSNLPDITGE 218
1 FASQYFMTLYKTYTYNVDGASFFNKLSFTTGLFGWGIRKALKQIIRSNLPDITGE - 59
OY 219 HVSRLQHTISSYKDYMDQTPALPKAKRSLSLVVQRLATVAGYDTPYKWKYMKLK 278
60 HPEATIREIASGEGYEMWTQVPAMTSFAERFSKMATKTLTVSDYVHLPAYKRWYRKFK 119
OY 279 NFMVNRVFIPTKFFNKIREPSK-ALKEKYSTDTKDLFENKIGQGTVDFINNEIRDPK 337
120 EFTYN-FTTDPKALIMKHVSQPVKATATKLVPEHROAIRVVOGSTKHIAN-GVRLAR 177
OY 338 ALKEKVSNDADLFENKI-----GQGTVDFINNEIRDPKALIRKYSTGAEDLFENKIG 391
178 MIKE-----PSQOIRREKLPYLSKAKGAVEHVVDKVK--SKTLKRAGESEESYSDDSE 228
OY 392 QGTVDFINNEIRDPKALIRKYSTGAEDLFENKIGQGTVDFINNEIRDPKALIRKYSTGAEDLFENKIG 439
229 -SEEBILKESQYNPAKSVASADKDEYLDYADMDALYKK--YMWVGVGVEIKD 280

RESULT 28

015708 PRELIMINARY: PRT: 282 AA.
ID 015708: PRT: 282 AA.

DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RHOPTRY ASSOCIATED PROTEIN-1 (FRAGMENT).
OS Babesia bigemina.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBI_TaxID=5866;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=98135662; PubMed=9476795;
RA Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT loci of Babesia bigemina.";
RL Mol. Biochem. Parasitol. 90:479-489(1997).
DR EMBL: AF014486; AAC47658.1; -.
DR InterPro: IPR004318; RAP-1.
DR Pfam: PF03085; RAP-1; 1.
FT NON_TER 1
SQ SEQUENCE 282 AA; 32569 MW; F5391A7DA7D49BEE CRC64;

Query Match 18.5%; Score 437.5; DB 5; Length 282;
Best Local Similarity 35.1%; Pred. No. 2.3e-21;
Matches 104; Conservative 59; Mismatches 102; Indels 31; Gaps 11;

OY 159 FASRYLYMATLYKTYTYNVDGASFFNKLSFTTGLFGWGIRKALKQIIRSNLPDITGE 218
1 FASQYFMTLYKTYTYNVDGASFFNKLSFTTGLFGWGIRKALKQIIRSNLPDITGE - 59
OY 219 HVSRLQHTISSYKDYMDQTPALPKAKRSLSLVVQRLATVAGYDTPYKWKYMKLK 278
60 HPEATIREIASGEGYEMWTQVPAMTSFAERFSKMATKTLTVSDYVHLPAYKRWYRKFK 119
OY 279 NFMVNRVFIPTKFFNKIREPSK-ALKEKYSTDTKDLFENKIGQGTVDFINNEIRDPK 337
120 EFTYN-FTTDPKALIMKHVSQPVKATATKLVPEHROAIRVVOGSTKHIAN-GVRLAR 177
OY 338 ALKEKVSNDADLFENKI-----GQGTVDFINNEIRDPKALIRKYSTGAEDLFENKIG 391
178 MIKE-----PSQOIRREKLPYLSKAKGAVEHVVDKVK--SKTLKRAGESEESYSDDSE 228
OY 392 QGTVDFINNEIRDPKALIRKYSTGAEDLFENKIGQGTVDFINNEIRDPKALIRKYSTGAEDLFENKIG 439
229 -SEEBILKESQYNPAKSVASADKDEYLDYADMDALYKK--YMWVGVGVEIKD 280

RESULT 29

09GUD9 PRELIMINARY: PRT: 301 AA.
ID 09GUD9: PRT: 301 AA.

DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE RAP-1 ALPHA-1 (FRAGMENT).
OS Babesia bigemina.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBI_TaxID=5866;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S2P;
RX MEDLINE=98135662; PubMed=9476795;
RA Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT loci of Babesia bigemina.";
RL Mol. Biochem. Parasitol. 90:479-489(1997).
DR EMBL: AF017287; AAC14905.1; -.
FT NON_TER 1
SQ SEQUENCE 301 AA; 33868 MW; B162189C9668FC6 CRC64;

Query Match 18.5%; Score 437.5; DB 5; Length 301;
Best Local Similarity 37.8%; Pred. No. 2.5e-21;
Matches 105; Conservative 47; Mismatches 97; Indels 29; Gaps 10;

OY 159 FASRYLYMATLYKTYTYNVDGASFFNKLSFTTGLFGWGIRKALKQIIRSNLPDITGE 218
1 FASQYFMTLYKTYTYNVDGASFFNKLSFTTGLFGWGIRKALKQIIRSNLPDITGE - 59
OY 219 HVSRLQHTISSYKDYMDQTPALPKAKRSLSLVVQRLATVAGYDTPYKWKYMKLK 278
60 HPEATIREIASGEGYEMWTQVPAMTSFAERFSKMATKTLTVSDYVHLPAYKRWYRKFK 119
OY 279 NFMVNRVFIPTKFFNKIREPSK-ALKEKYSTDTKDLFENKIGQGTVDFINNEIRDPK 337

DB	120	ETVAV-FTTDPRAKLIMKHVSQPVKTAATYKLVPEEHRQARNDVGGSTKHIAN-GVNDLAR	177
OY	338	ALKEKVSNDADKLEFNKI-----GQGVDFINNEIRD--PSKALIRKYSTGAEDLFENK	389
Db	178	MIKE-----PSQOIIIREKILPHYLSKAKGAVEHVKKKSVYPK---QKGDOPSEAVEET	230
OY	390	IGQGVDFINNEIRDPKALIRKYTE-----ADD	419
Db	231	VPSC--DSAEFTEFVEPEEYVDVATVTEGVNSKKVDAD	266
RESULT 30			
ID	O9GUND8	PRELIMINARY:	PRT: 304 AA.
AC	O9GUND8		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	RAP-1 ALPHA-1 (FRAGMENT).		
GN	RAP-1 ALPHA-1.		
OS	Babesia bigemina.		
OC	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.		
OX	NCBI_TaxID=5666;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-UYA;		
RX	MEDLINE=98135662; PubMed=9476795;		
RA	Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;		
RT	"Genetic variation in the diomorphic regions of RAP-1 genes and rap-1		
RL	loci of Babesia bigemina."		
DR	Mol. Biochem. Parasitol. 90:479-489(1997).		
FT	EMBL, AF017289; AAG14907.1; .		
FT	NON_TER		
SO	SEQUENCE 304 AA; 34195 MW; 046162DD5A48B8FE CRC64;		
Query Match	18.5%; Score 437.5; DB 5; Length 304;		
Best Local Similarity	36.5%; Pred. No. 2.6e-21;		
Matches 115; Conservative 51; Mismatches 116; Indels 33; Gaps 13			
OY	159	FASRLVYMATLVYKTYTNVDEFGASFPNKLSPFTTGLFGWIKRALKOIRSNLPLDIGTE	218
Db	1	FASQFYFWMTLVKYLYLVDFPAKAFPNKLATTRFLFGIGIKALKRLVRSNLPVDLGT	59
OY	219	HSVSKLQHTSSYKRYMDTOIPALPKFAKRSLSAVQRLATVAGYVDTPTWKWYMKIK	278
Db	60	HPEATIRREIASGCGYEMVQVPAKMSFARFESKMAKTLLVTVSDVHLPAVKRWRRKKK	119
OY	279	NEMVNRVFLPTKKFENKEIREPSK-ALKEKYSTDRKDLFENKIGQGVDFPFNKKEIRDPSK	337
Db	120	ETVAV-FTTDPRAKLIMKHVSQPVKTAATYKLVPEEHRQARNDVGGSTKHIAN-GVNDLAR	177
OY	338	ALKEKVSNDADKLEFNKI-----GQGVDFINNEIRD--PSKALIRKYSTGAEDLFENK	389
Db	178	MIKE-----PSQOIIIREKILPHYLPKAKGAVEHVKKKSVYPK---QKGDOPSEAVEET	230
OY	390	IGQGVDFINNEIRDPKALIRKYT-----EADDLFENKIGQGVDFINKEIR--D	439
Db	231	VPSC--DSAEFTEFVEPEEYVDVATVTEGVNSKKVDADDA-GNAETQQLPAEN-EVRAAD	286
OY	440	PSKALIRKYSTEADN	454
Db	287	PKNEDSSSSSSSSD	301
RESULT 31			
ID	O9GNIS	PRELIMINARY:	PRT: 263 AA.
AC	O9GNIS;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	RAP1 BETA-2 (FRAGMENT).		

Query Match	Best Local Similarity	18.5%;	Score 437;	DB 5;	Length 263;
Matches	99;	Conservative	50;	Mismatches	85;
159	FASRLVYATLYKYKTYTNDVDEGSAFFENKLSFTTGPGMGIRKAIKOIRSLPDLIGTE	1	1	1	1
1	FASQFTFTTLYKYKTYTNDVDEGSAFFENKLSFTTGPGMGIRKAIKOIRSLPDLIGT	1	1	1	1
219	HSVSLQHTTSYKDYMDTOIPALPKFKRSLSMVVORLLATVAGYVDPYWKYMKLK	1	1	1	1
60	HPEATIRELASGYGYMTQVDPAMTSFAERFSKMATKTLTVSDYVHLPAKRYRKFK	1	1	1	1
279	NEMVARYIPIPKKFKFKIREPSK-ALAEKYSTDRKDFENKIGGYTDFNFKEIRDSK	1	1	1	1
120	EFTVAFETDPKALIMKHVSQPKYATYKLVPEEHRQAIRDVGOSTHIAN-GVDDLAR	1	1	1	1
338	ALAEKVSNDANDLFEENKTI-----GGGTVDVFINEIRDPKSKALLIKVSTGAEDLLEN	1	1	1	1
178	MIKE-----PSQOILREKILPHLYSKRKAAGVENVYDKV--SKTLKKRAGSSSESYSDSEE	1	1	1	1
389	---KIGGCTVDFINNE 401	1	1	1	1
232	ELKESQYNSDREND 247	1	1	1	1
09GUD6	PRELIMINARY; PRT; 263 AA.	1	1	1	1
09GUD6	PRELIMINARY; PRT; 263 AA.	1	1	1	1
01-MAR-2001	(TREMUREL. 16, Created)	1	1	1	1
01-MAR-2001	(TREMUREL. 16, Last sequence update)	1	1	1	1
01-MAR-2001	(TREMUREL. 16, Last annotation update)	1	1	1	1
RAP1	BETA-2 (FRAGMENT).	1	1	1	1
RAP-1	BETA-2.	1	1	1	1
Babesia bigemina.		1	1	1	1
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesidae; Babesia.		1	1	1	1
NCBI_TaxID=5866;		1	1	1	1
SEQUENCE FROM N.A.		1	1	1	1
STRAIN=CGA;		1	1	1	1
MEDLINE=98135662; Pubmed=9476795;		1	1	1	1
Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;		1	1	1	1
"Genetic variation in the dimorphic regions of RAP-1 genes and rap-1		1	1	1	1
loci of Babesia bigemina."		1	1	1	1
Mol. Biochem. Parasitol. 90:479-489(1997).		1	1	1	1
EMBL; AF017293; AAC14911.1; -		1	1	1	1
EMBL; AF017292; AAC14910.1; -		1	1	1	1
NON_TER		1	1	1	1
SEQUENCE 263 AA; 30250 MW; 15B60C136417AD6B CXC64;		1	1	1	1
Query Match	Best Local Similarity	18.5%;	Score 437;	DB 5;	Length 263;
Matches	99;	Conservative	50;	Mismatches	85;
159	FASRLVYATLYKYKTYTNDVDEGSAFFENKLSFTTGPGMGIRKAIKOIRSLPDLIGTE	1	1	1	1
1	FASQFTFTTLYKYKTYTNDVDEGSAFFENKLSFTTGPGMGIRKAIKOIRSLPDLIGT	1	1	1	1
219	HSVSLQHTTSYKDYMDTOIPALPKFKRSLSMVVORLLATVAGYVDPYWKYMKLK	1	1	1	1
60	HPEATIRELASGYGYMTQVDPAMTSFAERFSKMATKTLTVSDYVHLPAKRYRKFK	1	1	1	1
279	NEMVARYIPIPKKFKFKIREPSK-ALAEKYSTDRKDFENKIGGYTDFNFKEIRDSK	1	1	1	1
120	EFTVAFETDPKALIMKHVSQPKYATYKLVPEEHRQAIRDVGOSTHIAN-GVDDLAR	1	1	1	1
338	ALAEKVSNDANDLFEENKTI-----GGGTVDVFINEIRDPKSKALLIKVSTGAEDLLEN	1	1	1	1
178	MIKE-----PSQOILREKILPHLYSKRKAAGVENVYDKV--SKTLKKRAGSSSESYSDSEE	1	1	1	1
389	---KIGGCTVDFINNE 401	1	1	1	1
232	ELKESQYNSDREND 247	1	1	1	1
09GUD6	PRELIMINARY; PRT; 263 AA.	1	1	1	1
09GUD6	PRELIMINARY; PRT; 263 AA.	1	1	1	1
01-MAR-2001	(TREMUREL. 16, Created)	1	1	1	1
01-MAR-2001	(TREMUREL. 16, Last sequence update)	1	1	1	1
01-MAR-2001	(TREMUREL. 16, Last annotation update)	1	1	1	1
RAP1	BETA-2 (FRAGMENT).	1	1	1	1
RAP-1	BETA-2.	1	1	1	1
Babesia bigemina.		1	1	1	1
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesidae; Babesia.		1	1	1	1
NCBI_TaxID=5866;		1	1	1	1
SEQUENCE FROM N.A.		1	1	1	1
STRAIN=CGA;		1	1	1	1
MEDLINE=98135662; Pubmed=9476795;		1	1	1	1
Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;		1	1	1	1
"Genetic variation in the dimorphic regions of RAP-1 genes and rap-1		1	1	1	1
loci of Babesia bigemina."		1	1	1	1
Mol. Biochem. Parasitol. 90					

